REMARKS

No amendments to the claims are made. Claims 1-28 are cancelled. Claims 29-40 are pending.

Attorney Docket Number

Please change the attorney docket number from "CL1792 USNA" to "2119-4268 (CL1792 USNA)".

Objections to the Specification

The title and abstract are amended as suggested by the Examiner. Support for the amendments can be found throughout the specification as filed. Applicants respectfully request withdrawal of the objection.

Written Description

Claims 35 and 39-40 are rejected under 35 U.S.C. § 112, first paragraph, written description. Applicants respectfully traverse.

The Examiner states that "Although a genus of regulatory sequences is known in the art, no description of a homologous regulatory sequence, that which is naturally linked to promote the expression of the gene, was in the possession of the inventors at the time of filing." (Office Action, page 4, lines 3-6).

Applicants submit that the subject matter of this application has been described in the specification to reasonably convey to one skilled in the relevant art that the inventors, at the

time the application was filed, had possession of the claimed invention. The Examiner's attention is directed to the specification as filed:

> "Promoter" refers to DNA sequence capable of controlling the expression of a coding sequence or functional RNA. In general, a coding sequence is located 3' to a promoter sequence. Promoters may be derived in their entirety from a native gene, or be composed of different elements derived from different promoters found in nature, or even comprise synthetic DNA segments. It is understood by those skilled in the art that different promoters may direct the expression of a gene in different tissues or cell types, or at different stages of development, or in response to different environmental conditions. Promoters which cause a gene to be expressed in most cell types at most times are commonly referred to as "constitutive promoters". It is further recognized that since in most cases the exact boundaries of regulatory sequences have not been completely defined, DNA fragments of different lengths may have identical promoter activity" (specification, page 14, line 31 through page 15, line 6).

Furthermore, the Examiner's attention is directed to the following:

> Both heterologous and non-heterologous (i.e., endogenous) promoters can be employed to direct expression of isopentenyl diphosphate pathway gene. These promoters can also be used, for example, in recombinant expression cassettes to drive expression of antisense nucleic acids to reduce, increase, or alter concentration and/or composition of the isopentenyl diphosphate pathway protein in a desired tissue. Thus, in some embodiments, the nucleic acid construct will comprise a promoter functional in a plant cell, such as in Zea mays or tobacco, operably linked to an isopentenyl diphosphate pathway biosynthetic gene. Gene promoters useful in these emodiments include the endogenous promoters driving expression of the isopentenyl diphosphate pathway proteins" (specification, page 24, line 34 through page 25, line 7).

In view of above discussion, Applicant believes sufficient relevant identifying characteristics have been disclosed to allow one skilled in the art to recognize the invention as claimed, and thereby meet the written description requirement. Therefore, Applicant respectfully requests withdrawal of the rejection.

Scope of Enablement

Claims 29-31 and 34-40 are rejected under 35 U.S.C. § 112, first paragraph, scope of enablement. Applicants respectfully traverse.

The Examiner concedes that the specification is enabling for polynucleotides encoding SEQ ID NO:8 having acetyl-CoA acetyltransferase activity. The Examiner also concedes that the art enables any DNA encoding SEQ ID NO:8 based on the degeneracy of the genetic code, and that the instant specification describes and enables means for identifying other acetyl-CoA acetyltransferase genes using hybridization methods. However, the Examiner asserts that the specification does not provide enablement for polynucleotides encoding polypeptides of varied sequence having this activity because "these methods do not enable one of skill in the art to make all, or a relevant portion of, the polynucleotides within the scope of the claims" (Office Action, page 6) because the ability to finad an acetyl-CoA acetyltransferase gene is not equivalent to the ability to make an acetyl-CoA acetyltransferase gene. The Examiner asserts that "No description in the specification or the art provides particular residues whose encoding is important within the disclosed sequence so that its acetyl-CoA acetyltransferase-nature is maintained" (Office Action, page 6). The Examiner asserts that undue experimentation would be required.

Applicants refer to Appendix A for a comparison of the claimed sequence with the sequence from *Zoogloea ramigera* (135759) disclosed by Palmer et al (J. Biol. Chem., 1991, 266: 8369-8375). This comparison demonstrates that the sequences share the conserved active site region, in particular the two active site cysteine residues. One skilled in the art would appreciate that the more highly conserved a residue is, the less likely that it could be modified

and function maintained. From the example set forth in Palmer et al and the attached alignment (Appendix A), one skilled in the art could quickly determine which amino acid residues might be modified in SEQ ID NO:8 without a likely change in function. Since SEQ ID NO:8 and the *Zoogloea* sequence share only 38.3% identity, one of skill in the art would have appreciated that many variants sharing at least 85% sequence identity to SEQ ID NO:8 would retain the claimed activity. Therefore, sufficient specific characteristics for the claimed sequence of SEQ ID NO:8 have been submitted.

CONCLUSION

Applicants thank the Examiner for the statement that the claimed subject matter is considered free of the prior art, and note that claims 32 and 33 are not rejected. Based on the foregoing amendments and remarks, Applicants respectfully request reconsideration and withdrawal of the rejection of claims and allowance of this application.

AUTHORIZATION

The Commissioner is hereby authorized to charge any additional fees which may be required for consideration of this Amendment to Deposit Account No. 13-4500, Order No. 2119-4268. A DUPLICATE OF THIS DOCUMENT IS ATTACHED.

In the event that an extension of time is required, or which may be required in addition to that requested in a petition for an extension of time, the Commissioner is requested to grant a petition for that extension of time which is required to make this response timely and is hereby authorized to charge any fee for such an extension of time or credit any overpayment for an extension of time to Deposit Account No. 13-4500, Order No. 2119-4268. A DUPLICATE OF THIS DOCUMENT IS ATTACHED.

Respectfully submitted,
MORGAN & FINNEGAN, L.L.P.

Dated: August 6, 2004

By: 

Michael A. Willis
Registration No. 53,913

Correspondence Address:
MORGAN & FINNEGAN, L.L.P.
Three World Financial Center
New York, NY 10281-2101

(212) 415-8700 Telephone
(212) 415-8701 Facsimile

APPENDIX A

Comparison of the amino acid sequences of the Acetyl-CoA acetyltransferases from *Hevea brasiliensis* clone with SID NO: ehb2c.pk006.05 (SEQ ID NO:8) and *Zoogloea ramigera* set forth in NCBI General Identifier No.:135759. Amino acids conserved among the two sequences are indicated with an asterix above the conserved residues. Dashes are used by the program to maximize alignment of the sequences. Residues found to be conserved in all thiolase sequences including the active site residues cysteine (•) are underlined (Palmer et al. 1991, J. Biol.Chem. 266: 8369-8375).

```
             **  *             ***  * * *      *  **   * * * ** *    * **
GI:135759    MSTPSI--------VIASARTAVGSFNGAFANTPAHELGATVISAVLERAGVAAGEVNEV
SEQ ID NO:8  MSPSSDSINPRDVCIVGVARTPMGGFLGSLSSFSATKLGSIAIQAALKRANVDPSLVQEV
               * *  *  ** ******  ** *        *  * **  *  *    *  *   * *
GI:135759    ILGQVLPAGEGQNPARQAAMKAGVPQEATAWGMNQLCGSGLRAVALGMQQIATGDASIIV
SEQ ID NO:8  FFGNVLSANLGQAPARQAALGAGIPNSVICTTINKVCASGMKATMLAALTIQVGINDIVV
                                                 •
             ******** **   *    *   *    ** * **** *      **  **  * *
GI:135759    AGGMESMSMAPHC-AHLAGGVKMGDFKMIDTMIKDGLTDAFYGYHMGTTAENVAKQWQLS
SEQ ID NO:8  AGGMESMSNAPKYLAEARRGSRLGHDTIIDGMLKDGLWDVYNDFGMGVCAEICADQHNIT
             * * *  *  *      **  * *  ****  * *  *     ** **  *   *
GI:135759    RDEQDAFAVASQNKAEAAQKDGRFKDEIVPFIVKGRKGD--ITVDADE-YIRHGATLDSM
SEQ ID NO:8  REEKDSYAIRSFERGNSAQNGGVFSWEIVPVEVSGGRGKSVMVVDKDEGLIKFDAA--KL
              ****     * *******   *****  * *   *   * *   **          *
GI:135759    AKLRPAFDKEGTVTAGNASGLNDGAAAALLMSEAEASRRGIQPLGRIVSWATVGVDPKVM
SEQ ID NO:8  RKLRP-ISRIGSVTAGNASIISDGAAALVLVSGEKAIELGLQVIARIRGYGDAAQAPELF
              * *  *  **   **      *  * ****   * *  * **  *   ** ***   **
GI:135759    GTGPIPASRKALERAGWKIGDLDLVEANEAFAAQACAVNKDLGWDPSIVNVNGGAIAIGH
SEQ ID NO:8  TTAPALAIPKAISNAGLEASQIDYYEINEAFSVVALANQKILGLNPEKLNVHGGAVSLGH
             * * ****** ***          * *  * ***   *   *           L
GI:135759    PIGASGARILNTLLFEMKRRGARKGLATLCIGGGMGVAMCIES----------L
SEQ ID NO:8  PLGCSGARILVTLLGVLRHKNGKYGVASICNGGGGASALVLELMSVGRVGRSLL
                                      •
```